SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Wolf, Marcia K
                  Cassels, Fred J
                  Boedeker, Edgar C

    (ii) TITLE OF INVENTION: Transformed Bacteria Producing GS6
            Antigens as Vaccines

   (iii) NUMBER OF SEQUENCES: 10

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Hendricks and Assoc
        (B) STREET: P.O. Box 2509
        (C) CITY: Fairfax
        (D) STATE: VA
        (E) COUNTRY: US
        (F) ZIP: 22031

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 09/479,877
        (B) FILING DATE: 10-JAN-2000
        (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Hendricks, Glenna M
        (B) REGISTRATION NUMBER: 32,535

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 703/425-8405
        (B) TELEFAX: 703/425-8406

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4875 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTGTAA CCAGTTGATA AAAATATATC ACGCTGGGAA TGACGTGATG TATATACGGA   60

GCAGCTATGT CGGAACAGAT ATTTTCCTAT CGGTATGCGT TGTGAGTAAG CGTAAAGCCA   120

ATGCTGTCTG TAACTCCTGA TCCTTGCAGA CTAAATTAGA GCTCCTTCTA AATTAGACGG   180

ATGGATAAAC CTACAGACTG GCGCTCTGGG TCTCGCCGGA TATTTTCTAA TGAATTTAAG   240

CTTCATATGG TTGAACTGGC TTCGAAACCA AATGCCAATG TCGCACAACT GGCTCGGGAA   300

CATGGCGTTG ATAACAACCT GATTTTTAAA TAGCTACGCC TCTGGCAAAG AGAAGGACGT   360

ATTTCTCGTA GAATGCCTCC AACTATTGTA GGCCCTACAG TACCACTGAG GTAGCCTGAA   420

TTTAAAGCCG AAGCGGTCAG AACTGTTCTT GGTGTGAACG TAGCACTCAC CAATAAAAGC   480

ATCAATACGG TGCTCTGTTG ACACATTACG AATGTTATGT ATACAATAAA AATGATTATA   540

GCAATATTAA TGGTGTTATA TGAAGAAAC AATTGGTTTA ATTCTAATTC TTGCTTCATT   600

CGGCAGCCAT GCCAGAACAG AAATAGCGAC TAAAAACTTC CCAGTATCAA CGACTATTTC   660

AAAAAGTTTT TTTGCACCTG AACCACGAAT ACAGCCTTCT TTTGGTGAAA ATGTTGGAAA   720

GGAAGGAGCT TTATTATTTA GTGTGAACTT AACTGTTCCT GAAAATGTAT CCCAGGTAAC   780

GGTCTACCCT GTTTATGATG AAGATTATGG GTTAGGACGA CTAGTAAATA CCGCTGATGC   840

TTCCCAATCA ATAATCTACC AGATTGTTGA TGAGAAGGG AAAAAAATGT TAAAAGATCA   900

TGGTGCAGAG GTTACACCTA ATCAACAAT AACTTTTAAA GCGCTGAATT ATACTAGCGG   960

GGAAAAAAAA ATATCTCCTG GAATATATAA CGATCAGGTT ATGGTTGGTT ACTATGTAAA   1020

CTAAATACTG GAAGTATGAT TATGTTGAAA AAAATTATTT CGGCTATTGC ATTAATTGCA   1080

GGAACTTCCG GAGTGGTAAA TGCAGGAAAC TGGCAATATA AATCTCTGGA TGTAAATGTA   1140

AATATTGAGC AAAATTTTAT TCCAGATATT GATTCCGCTG TTCGTATAAT ACCTGTTAAT   1200

TACGATTCGG ACCCGAAACT GGATTCACAG TTATATACGG TTGAGATGAC GATCCCTGCA   1260

GGTGTAAGCG CAGTTAAAAT CGCACCAACA GATAGTCTGA CATCTTCTGG ACAGCAGATC   1320

GGAAAGCTGG TTAATGTAAA CAATCCAGAT CAAAATATGA ATTATTATAT CAGAAAGGAT   1380

TCTGGCGCTG GTAACTTTAT GGCAGGACAA AAAGGATCCT TTCCTGTCAA AGAGAATACG   1440

TCATACACAT TCTCAGCAAT TTATACTGGT GGCGAATACC CTAATAGCGG ATATTCGTCT   1500

```
GGTACTTATG CAGGAAATTT GACTGTATCA TTTTACAGCA ATTAAAAAAA GGCCGCATTA    1560

TTGCGGCCAT TGACGATACT GCTAGGCAAA AATATGAAAT CAAAGTTAAT TATACTATTG    1620

ACGTTAGTGC CATTTTCATC TTTTTCAACA GGAAATAATT TTGAAATAAA TAAGACACGA    1680

GTAATTTACT CTGACAGCAC ACCATCAGTT CAAATATCAA ATAATAAAGC ATATCCTTTA    1740

ATTATTCAAA GCAATGTATG GGATGAAAGC AATAATAAAA TCATGACTT TATAGCAACA      1800

CCACCGATTT TTAAAATGGA AAGTGAAAGT CGGAATATAA TAAAAATAAT TAAAACAACT    1860

ATTAATTTGC CGGACTCTCA GGAAAGTATG AGATGGTTAT GTATTGAATC AATGCCACCA    1920

ATAGAAAAAA GTACTAAAAT AAACAGAAAA GAAGGAAGGA CAGACAGTAT TAATATCAGC    1980

ATTCGGGGGT GCATTAAACT GATATATCGA CCTGCCAGTG TTCCGTCTCC TGTTTTTAAT    2040

AATATAGTAG AAAAATTAAA ATGGCATAAA AATGGAAAGT ATCTTGTATT AAAAAATAAT    2100

ACACCCTATT ACATTAGCTT TTCTGAGGTT TTTTTTGATT CAGATAAAGT AAACAATGCA    2160

AAAGATATTT TATATGTAAA ACCATACTCA GAGAAGAAAA TAGATATCAG CAACAGAATA    2220

ATAAAAAAAA TCAAATGGGC TATGATTGAT GATGCTGGCG CAAAAACAAA ACTTTATGAA    2280

TCAATTTTAT AAAAAATCTC ATTACAGTAT ACAAAAACAT CAGATTACAG GCTTGCTTTT    2340

TTTGCTATTT ATATATCCTT TCTCAACCTC ATATGGAAAT GAACAATTTA GTTTTGACTC    2400

ACGATTCCTA CCATCAGGTT ATAATTACTC TTTAAATAGT AACTTACCTC CTGAAGGTGA    2460

GTATCTGGTT GATATTTATA TTAACAAAAT AAAAAAGGAG TCCGCGATTA TTCCTTTTTA    2520

TATAAAAGGA AATAAACTTG TACCATGTTT ATCAAAAGAA AAAATTTCAT CTTTGGGTAT    2580

CAACATTAAT AATAACGACA ACACAGAGTG TGTAGAAACA AGTAAGGCAG GTATTAGTAA    2640

TATCAGCTTT GAGTTTAGCT CTCTTCGTTT GTTTATTGCT GTACCGAAAA ATCTTCTGTC    2700

TGAGATTGAT AAAATATCAT CAAAGGATAT AGATAACGGG ATTCATGCTT TATTTTTTAA    2760

TTATCAAGTA AATACAAGGC TAGCCAATAA TAAAAATCGT TATGATTACA TTTCTGTTTC    2820

ACCAAATATA AATTATTTTT CATGGCGGTT GCGTAATCTT TTTGAATTTA ACCAAAACAA    2880

CGATGAAAAA ACATGGGAAA GAAACTACAC TTATCTAGAA AAAGTTTTT ATGATAAAAA      2940

GCTAAACTTA GTCGTTGGTG AAAGTTATAC GAATTCAAAT GTTTATAATA ACTACTCTTT    3000

TACTGGTATT TCAGTTTCTA CAGATACAGA TATGTATACG CCAAGTGAAA TCGATTATAC    3060

ACCAGAAATT CATGGAGTGG CTGATTCAGA CTCTCAGATT ATTGTCAGGC AAGGCAACAC    3120
```

```
CATTATCATT AATGAAAGTG TTCCAGCCGG ACCGTTCTCA TTTCCAATAA CCAATCTCAT      3180

GTATACTGGG GGGCAACTTA ATGTGGAGAT AACAGATATT TATGGAAATA AAAAACAATA      3240

TACTGTCAAT AATTCCTCTC TTCCTGTTAT GAGAAAAGCG GGACTAATGG TATATAATTT      3300

TATATCTGGG AAATTAACAA AAAAAAATAG TGAGGATGGT GATTTTTTTA CTCAAGGTGA      3360

TATTAACTAC GGTACTCACT ATAACAGCAC ACTATTCGGT GGATATCAGT TTAGTAAAAA      3420

TTATTTTAAC TTATCTACTG GTATAGGCAC TGATCTGGGA TTTTCTGGAG CATGGCTACT      3480

ACACGTTAGC AGAAGTAATT TTAAGAATAA AAATGGATAT AATATTAATC TACAACAAAA      3540

CACTCAGTTA AGACCATTCA ATGCCGGGGT TAATTTCGAT TACGCATACA GAAAAAAAAG      3600

GTATGTGGAA CTTTCCGACA TTGGCTGGCA TGGTAATTTA TATAATCAAC TTAAAAATAG      3660

TTTTTCTTTA TCCTTGTCAA AATCATTGAA TAAATACGGA AATTTCTCAC TTGATTATAA      3720

CAAAATGAAA TACTGGGATA ATGCGTATGA TAGTAACTCA ATGTCGATTC GTTATTTTTT      3780

TAAATTCATG CGAGCAATGA TTACAACAAA TTGTTCTTTA AATAAATATC AATCTTATGA      3840

AAAAAAAGAT AAAAGATTTA GTATTAATAT ATCATTGCCT TTAACCAAAG ATTACGGGCA      3900

CATATCTTCA AACTATTCAT TTTCCAATGC AAATACAGGA ACGGCAACCA GTTCTGTAGG      3960

CTTAAACGGT AGTTTTTTTA ATGACGCAAG ATTAAACTGG AACATTCAGC AGAACAGAAC      4020

GACCCGTAAC AATGGATATA CTGATAATAC CAGTTACATA GCAACCAGCT ATGCCTCTCC      4080

CTATGGCGTT TTTACTGGTT CATATTCAGG ATCGAACAAG TATTCAAGCC AGTTTTATTC      4140

TGCATCGGGA GGTATTGTTT TGCATAGCGA TGGCGTAGCT TTTACTCAAA AAGCCGGAGA      4200

TACCTCTGCT CTTGTCCGTA TTGATAATAT TTCTGATATA AAAATTGGTA ACACTCCTGG      4260

TGTTTATACT GGGTATAATG GTTTTGCTTT AATTCCTCAT CTTCAGCCGT TCAAAAAAAA      4320

CACCATTTTA ATTAATGATA AAGGAATTCC AGACGGTATT ACTCTTGCTA ATATAAAAAA      4380

ACAAGTTATC CCATCACGAG GAGCTATTGT TAAAGTAAAA TTTGATGCTA AAAAAGGCAA      4440

TGACATTTTG TTTAAGCTTA CAACTAAAGA TGGAAAAACG CCCCCATTAG GAGCTATAGC      4500

CCATGAAAAA AATGGAAAAC AGATTAATAC GGGTATCGTT GACGATGATG GTATGCTTTA      4560

TATGTCTGGA TTATCAGGGA CAGGGATTAT TAATGTAACA TGGAATGGAA AAGTCTGTTC      4620

ATTTCCTTTT TCAGAAAAAG ATATATCTAG CAAACAATTA TCTGTTGTAA ATAAACAATG      4680

TTAGGTAGTG CATCCAATTA GTAGAACATG TGTTTTTCGA TAAACGCTCC GATCTCTTTT      4740
```

TCGTGGATCT CAACTGAGCG TGAGAAGCAG ATTGTTTTAC GAGCCAACCG CTTAATGCGG   4800

GTGCGTAGCG TCAGATTATT ACGCTCAATG CGTTGGGTGA ATATTTTGCC GGTCAGATGC   4860

TTATTCTTCG GTACC   4875

(2) INFORMATION FOR SEQ ID NO:2:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCCGCATTA TTGCGGCC   18

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCGCATTA TTGATTGCGG CC   22

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 527 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
TTGACACATT ACGAATGTTA TGTATACAAT AAAAATGATT ATAGCAATAT TAATGGTGTT      60

ATATGAAGAA AACAATTGGT TTAATTCTAA TTCTTGCTTC ATTCGGCAGC CATGCCAGAA     120

CAGAAATAGC GACTAAAAAC TTCCCAGTAT CAACGACTAT TTCAAAAAGT TTTTTTGCAC     180

CTGAACCACG AATACAGCCT TCTTTTGGTG AAAATGTTGG AAAGGAAGGA GCTTTATTAT     240

TTAGTGTGAA CTTAACTGTT CCTGAAAATG TATCCCAGGT AACGGTCTAC CCTGTTTATG     300

ATGAAGATTA TGGGTTAGGA CGACTAGTAA ATACCGCTGA TGCTTCCCAA TCAATAATCT     360

ACCAGATTGT TGATGAGAAA GGGAAAAAAA TGTTAAAAGA TCATGGTGCA GAGGTTACAC     420

CTAATCAACA AATAACTTTT AAAGCGCTGA ATTATACTAG CGGGGAAAAA AAAATATCTC     480

CTGGAATATA TAACGATCAG GTTATGGTTG GTTACTATGT AAACTAA               527
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 154 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: peptide

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Lys Lys Thr Ile Gly Leu Ile Leu Ile Leu Ala Ser Phe Gly Ser
1               5                  10                  15


His Ala Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr
            20                  25                  30


Ile Ser Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe
        35                  40                  45


Gly Glu Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu
    50                  55                  60
```

```
Thr Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp
65              70              75                      80

Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln
            85              90                      95

Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys
            100             105                     110

Asp His Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala
        115             120             125

Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn
    130             135                 140

Asp Gln Val Met Val Gly Tyr Tyr Val Asn
145             150
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 167 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: peptide

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Leu Lys Lys Ile Ile Ser Ala Ile Ala Leu Ile Ala Gly Thr Ser
1               5               10                      15

Gly Val Val Asn Ala Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn
            20              25                      30

Val Asn Ile Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg
        35              40                      45

Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu
    50              55                      60
```

```
Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile
65              70              75              80

Ala Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu
            85              90              95

Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys
        100             105             110

Asp Ser Gly Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro
        115             120             125

Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly
    130             135             140

Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu
145             150             155             160

Thr Val Ser Phe Tyr Ser Asn
            165
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 212 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: peptide

  (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Asn Asn Phe Glu Ile Asn Lys Thr Arg Val Ile Tyr Ser Asp Ser Thr
1               5               10              15

Pro Ser Val Gln Ile Ser Asn Asn Lys Ala Tyr Pro Leu Ile Ile Gln
            20              25              30

Ser Asn Val Trp Asp Glu Ser Asn Asn Lys Asn His Asp Phe Ile Ala
        35              40              45
```

```
Thr Pro Pro Ile Phe Lys Met Glu Ser Glu Ser Arg Asn Ile Ile Lys
    50          55              60

Ile Ile Lys Thr Thr Ile Asn Leu Pro Asp Ser Gln Glu Ser Met Arg
65              70              75                      80

Trp Leu Cys Ile Glu Ser Met Pro Pro Ile Glu Lys Ser Thr Lys Ile
                85              90                      95

Asn Arg Lys Glu Gly Arg Thr Asp Ser Ile Asn Ile Ser Ile Arg Gly
            100             105             110

Cys Ile Lys Leu Ile Tyr Arg Pro Ala Ser Val Pro Ser Pro Val Phe
            115             120             125

Asn Asn Ile Val Glu Lys Leu Lys Trp His Lys Asn Gly Lys Tyr Leu
    130             135             140

Val Leu Lys Asn Asn Thr Pro Tyr Tyr Ile Ser Phe Ser Glu Val Phe
145             150             155                     160

Phe Asp Ser Asp Lys Val Asn Asn Ala Lys Asp Ile Leu Tyr Val Lys
            165             170             175

Pro Tyr Ser Glu Lys Lys Ile Asp Ile Ser Asn Arg Ile Ile Lys Lys
            180             185             190

Ile Lys Trp Ala Met Ile Asp Asp Ala Gly Ala Lys Thr Lys Leu Tyr
        195             200             205

Glu Ser Ile Leu
    210
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 802 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: peptide

   (iii) HYPOTHETICAL: NO

```
Met Asn Gln Phe Tyr Lys Lys Ser His Tyr Ser Ile Gln Lys His Gln
1               5               10              15

Ile Thr Gly Leu Leu Phe Leu Leu Phe Ile Tyr Pro Phe Ser Thr Ser
            20              25              30

Tyr Gly Asn Glu Gln Phe Ser Phe Asp Ser Arg Phe Leu Pro Ser Gly
            35              40              45

Tyr Asn Tyr Ser Leu Asn Ser Asn Leu Pro Pro Glu Gly Glu Tyr Leu
    50              55              60

Val Asp Ile Tyr Ile Asn Lys Ile Lys Lys Glu Ser Ala Ile Ile Pro
65              70              75              80

Phe Tyr Ile Lys Gly Asn Lys Leu Val Pro Cys Leu Ser Lys Glu Lys
            85              90              95

Ile Ser Ser Leu Gly Ile Asn Ile Asn Asn Asn Asp Asn Thr Glu Cys
            100             105             110

Val Glu Thr Ser Lys Ala Gly Ile Ser Asn Ile Ser Phe Glu Phe Ser
            115             120             125

Ser Leu Arg Leu Phe Ile Ala Val Pro Lys Asn Leu Leu Ser Glu Ile
    130             135             140

Asp Lys Ile Ser Ser Lys Asp Ile Asp Asn Gly Ile His Ala Leu Phe
145             150             155             160

Phe Asn Tyr Gln Val Asn Thr Arg Leu Ala Asn Asn Lys Asn Arg Tyr
            165             170             175

Asp Tyr Ile Ser Val Ser Pro Asn Ile Asn Tyr Phe Ser Trp Arg Leu
            180             185             190

Arg Asn Leu Phe Glu Phe Asn Gln Asn Asn Asp Glu Lys Thr Trp Glu
    195             200             205
```

```
Arg Asn Tyr Thr Tyr Leu Glu Lys Ser Phe Tyr Asp Lys Lys Leu Asn
    210             215             220

Leu Val Val Gly Glu Ser Tyr Thr Asn Ser Asn Val Tyr Asn Asn Tyr
225             230             235             240

Ser Phe Thr Gly Ile Ser Val Ser Thr Asp Thr Asp Met Tyr Thr Pro
            245             250             255

Ser Glu Ile Asp Tyr Thr Pro Glu Ile His Gly Val Ala Asp Ser Asp
            260             265             270

Ser Gln Ile Ile Val Arg Gln Gly Asn Thr Ile Ile Ile Asn Glu Ser
        275             280             285

Val Pro Ala Gly Pro Phe Ser Phe Pro Ile Thr Asn Leu Met Tyr Thr
    290             295             300

Gly Gly Gln Leu Asn Val Glu Ile Thr Asp Ile Tyr Gly Asn Lys Lys
305             310             315             320

Gln Tyr Thr Val Asn Asn Ser Ser Leu Pro Val Met Arg Lys Ala Gly
            325             330             335

Leu Met Val Tyr Asn Phe Ile Ser Gly Lys Leu Thr Lys Lys Asn Ser
        340             345             350

Glu Asp Gly Asp Phe Phe Thr Gln Gly Asp Ile Asn Tyr Gly Thr His
    355             360             365

Tyr Asn Ser Thr Leu Phe Gly Gly Tyr Gln Phe Ser Lys Asn Tyr Phe
    370             375             380

Asn Leu Ser Thr Gly Ile Gly Thr Asp Leu Gly Phe Ser Gly Ala Trp
385             390             395             400

Leu Leu His Val Ser Arg Ser Asn Phe Lys Asn Lys Asn Gly Tyr Asn
            405             410             415

Ile Asn Leu Gln Gln Asn Thr Gln Leu Arg Pro Phe Asn Ala Gly Val
        420             425             430
```

```
Asn Phe Asp Tyr Ala Tyr Arg Lys Lys Arg Tyr Val Glu Leu Ser Asp
        435             440             445

Ile Gly Trp His Gly Asn Leu Tyr Asn Gln Leu Lys Asn Ser Phe Ser
        450             455             460

Leu Ser Leu Ser Lys Ser Leu Asn Lys Tyr Gly Asn Phe Ser Leu Asp
465             470             475             480
Tyr Asn Lys Met Lys Tyr Trp Asp Asn Ala Tyr Asp Ser Asn Ser Met
                485             490             495

Ser Ile Arg Tyr Phe Phe Lys Phe Met Arg Ala Met Ile Thr Thr Asn
            500             505             510

Cys Ser Leu Asn Lys Tyr Gln Ser Tyr Glu Lys Lys Asp Lys Arg Phe
            515             520             525

Ser Ile Asn Ile Ser Leu Pro Leu Thr Lys Asp Tyr Gly His Ile Ser
    530             535             540

Ser Asn Tyr Ser Phe Ser Asn Ala Asn Thr Gly Thr Ala Thr Ser Ser
545             550             555             560

Val Gly Leu Asn Gly Ser Phe Phe Asn Asp Ala Arg Leu Asn Trp Asn
            565             570             575

Ile Gln Gln Asn Arg Thr Thr Arg Asn Asn Gly Tyr Thr Asp Asn Thr
            580             585             590

Ser Tyr Ile Ala Thr Ser Tyr Ala Ser Pro Tyr Gly Val Phe Thr Gly
        595             600             605

Ser Tyr Ser Gly Ser Asn Lys Tyr Ser Ser Gln Phe Tyr Ser Ala Ser
    610             615             620

Gly Gly Ile Val Leu His Ser Asp Gly Val Ala Phe Thr Gln Lys Ala
625             630             635             640

Gly Asp Thr Ser Ala Leu Val Arg Ile Asp Asn Ile Ser Asp Ile Lys
            645             650             655
```

```
Ile Gly Asn Thr Pro Gly Val Tyr Thr Gly Tyr Asn Gly Phe Ala Leu
            660             665             670

Ile Pro His Leu Gln Pro Phe Lys Lys Asn Thr Ile Leu Ile Asn Asp
            675             680             685

Lys Gly Ile Pro Asp Gly Ile Thr Leu Ala Asn Ile Lys Lys Gln Val
            690             695             700

Ile Pro Ser Arg Gly Ala Ile Val Lys Val Lys Phe Asp Ala Lys Lys
705             710             715             720

Gly Asn Asp Ile Leu Phe Lys Leu Thr Thr Lys Asp Gly Lys Thr Pro
            725             730             735

Pro Leu Gly Ala Ile Ala His Glu Lys Asn Gly Lys Gln Ile Asn Thr
            740             745             750

Gly Ile Val Asp Asp Asp Gly Met Leu Tyr Met Ser Gly Leu Ser Gly
            755             760             765

Thr Gly Ile Ile Asn Val Thr Trp Asn Gly Lys Val Cys Ser Phe Pro
770             775             780

Phe Ser Glu Lys Asp Ile Ser Ser Lys Gln Leu Ser Val Val Asn Lys
785             790             795             800

Gln Cys
```

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 136 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: peptide

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile Ser
1               5               10              15

Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe Gly Glu
        20              25              30

Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu Thr Val
        35              40              45

Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp
    50              55              60

Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln Ser Ile
65              70              75              80

Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys Asp His
            85              90              95

Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn
        100             105             110

Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn Asp Gln
        115             120             125

Val Met Val Gly Tyr Tyr Val Asn
    130             135
```

(2) INFORMATION FOR SEQ ID NO:10:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 146 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: unknown

   (ii) MOLECULE TYPE: peptide

 (iii) HYPOTHETICAL: NO

  (iv) ANTI-SENSE: NO

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln
1               5               10              15
```

Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn
            20   25   30

Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val Glu Met
            35   40   45

Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr Asp Ser
    50   55   60

Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn
65   70   75   80

Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly
                85   90   95

Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr
            100   105   110

Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser
        115   120   125

Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser Phe Tyr
    130   135   140

Ser Asn
145